



Blast 2 Sequences results

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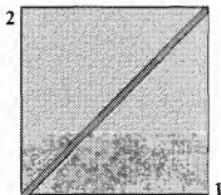
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix **BLOSUM62** gap open:**11** gap extension:**1**
x_dropoff: **0** expect: **10.0000** wordsize: **3** Filter View option **Standard**
Masking character option **X** for protein, **n** for nucleotide Masking color option **Black**
 Show CDS translation **Align**

Sequence 1: results for sequence "sin2" starting "AspIleValMet"

Length = 108 (1 .. 108)

Sequence 2: results for sequence "sin4" starting "AspIleLeuMet"
Length = 108 (1 .. 108)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score =	178 bits (452),	Expect =	9e-44
Identities =	86/108 (79%),	Positives =	96/108 (88%), Gaps = 0/108 (0%)
Query 1	DIVMTQSHKFMSTSVDGRVSITCKASQDVSTAVAWYQQKPGQSPKLIIYSASYRYTGVPA	CDR1	CDR2
DI+MTQS	KFMSTSVDGRVS+TCKASQ+V	VAVWYQQKPGQSPK	LIVSASYRY+GVP
Sbjct 1	DILMTQSQKFMSTSVDGRVSITCKASQNVGINVAWYQQKPGQSPKALIYSASYRYSVPD	CDR3	CDR4
Query 61	RFGSGSGSGTDFFTFTISSLVQTEDLAVYYCQQHYRTPPPTFGGGTKLELKR	108	
RF+GSGSGTDFT	TIS+VQ+EDLA Y+CQO+ P	TFGGGTKLE+KR	
Sbjct 61	RFTGSGSGTDFITLISNVQSEDIAEYFCQQYNSYPLTFGGGTKLEIKR	108	CDR3

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.



Blast 2 Sequences results

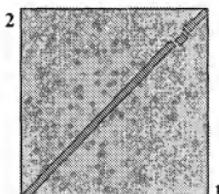
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Matrix **BLOSUM62** gap open:**11** gap extension:**1**x-dropoff: **0** expect: **10.000** wordsize: **3** Filter View option **Standard**
Masking character option X for protein, n for nucleotide Masking color option **Black**
 Show CDS translation **Align**

Sequence 1: results for sequence "sin1" starting "GlnValGlnLeu"
Length = 120 (1 .. 120)

Sequence 2: results for sequence "sin3" starting "GlnValGlnLeu"
Length = 119 (1 .. 119)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

		Score = 157 bits (396), Expect = 3e-37	
		Identities = 79/122 (64%), Positives = 94/122 (77%), Gaps = 5/122 (4%)	
Query	Subject	Cle1 (Dc2)	
Query 1	QVQLKQSGAELVRPGASVRLSCKASGYTFTYWINNIKWRPEQGLEWIGRIDPYDSETRY	60	
	QVQL+QSG EL +PGASV++SCKASGY+F+ Y +NN+KQ + LEWIG IDPY+ + T Y		
Sbjct 1	QVQLQQSGPPELEKPGASVKISCKASGYSPSDYNMNNVKQSNGKSLEWIGNIDPYNGDTNY	60	
	QVQLQQSGPPELEKPGASVKISCKASGYSPSDYNMNNVKQSNGKSLEWIGNIDPYNGDTNY		
Query 61	NQKFKD[KAILTVDKYSSTAYMQLSSLTSEDSAVYVCAKGVYDGHWF--FDVWGAGTSVTW	118	
	NQKFK[KA LT+DK SSTAYMQL SLTSEDSAVY+CA+W F WG GT VTV		
Sbjct 61	NQKFKG[KATLTDKSSSTAYMQLKSLSLTSSEDAVYFCAR--SRGWLLPPFAYWGQGTLVTW	117	
Query 119	SS 120		
	S+		
Sbjct 118	SA 119		

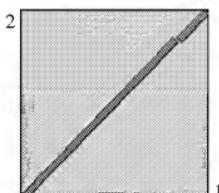
CPU time: 0.04 user secs. 0.04 sys. secs 0.08 total secs.

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
 x-dropoff: 0 expect: 10.0000 wordsize: 3 Filter View option: Standard
 Masking character option: X for protein, n for nucleotide Masking color option: Black
 Show CDS translation Align

Sequence 1: results for sequence "sin7" starting "GlnValGlnLeu"
 Length = 119 (1 .. 119)

Sequence 2: results for sequence "sin25" starting "GluValGlnLeu"
 Length = 117 (1 .. 117)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 159 bits (402), Expect = 6e-38
 Identities = 77/119 (64%), Positives = 95/119 (79%), Gaps = 2/119 (1%)

Query 1	QVQLQQSGGELVRPGTSVKVSKASGYAFTNYLIEWIRQRPGGLEIWIGVINPGGSNSKS	60
	+VVLQQQSG ELVRPG SVK+SCK S Y FT+Y + W++Q + LEWIGVI+ GN K	
Sbjct 1	EVQLQQSGPELVRPGVSVKISCKGSSYKFTDYAMHWVKQSHAKSLEWIGVISTYYGNVKY	60
Query 61	SKNLKGKATLTADKSSNTAYMQLSSLTSDSAAVYFCARSGVYGSSPDYWGQGTTLVSS	119
	++ KGKAT+T DKSS+TAYM+L+ LTS+DSA VY+CARS YGS DYWGQGT++TVSS	
Sbjct 61	NQKFKGKATMVDKSSSTAYMELARLTS EDSAVYCCARS--YGSYLDYWGQGTSVTVSS	117

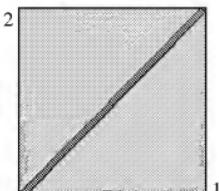
CPU time: 0.04 user secs. 0.04 sys. secs 0.08 total secs.

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Matrix: BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter View option: Standard
 Masking character option: X for protein, n for nucleotide Masking color option: Black
 Show CDS translation Align

Sequence 1: results for sequence "sin8" starting "AspValValMet"
 Length = 113 (1 .. 113)

Sequence 2: results for sequence "sin26" starting "AspIleValMet"
 Length = 112 (1 .. 112)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 227 bits (579), Expect = 2e-58
 Identities = 110/112 (98%), Positives = 111/112 (99%), Gaps = 0/112 (0%)

Query 1	DVVMTQTPLTLSTVTIGQPASISCKSSQSLDDSDGKTYLNWLLQPGQSPKRLIYLVSKLD	60
	D+VMTQTPLTLSTVTIGQPASISCKSSQSLDDSDGKTYLNWLLQPGQSPKRLIYLVSKLD	
Sbjct 1	DIVMTQTPLTLSTVTIGQPASISCKSSQSLDDSDGKTYLNWLLQPGQSPKRLIYLVSKLD	60
Query 61	SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWFQTHFPQTFGGGTKLEIK	112
	SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWFQTHFP	
Sbjct 61	SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWFQTHFPWTGGGTKEIK	112

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.